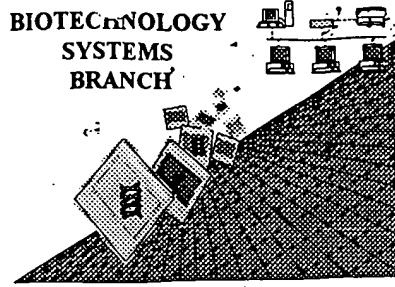


RAW SEQUENCE LISTING

ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/820,339

Source: OIPR

Date Processed by STIC: 2/27/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/820,339</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input checked="" type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/820,339

DATE: 07/27/2001
 TIME: 14:22:07

Input Set : A:\ES.txt
 Output Set: N:\CRF3\07272001\I820339.raw

Does Not Comply
 Corrected Diskette Needed

pn 4-5

3 <110> APPLICANT: FUCHS, Sara
 4 BARCHAN, Dora
 5 SOUROJON, Miriam
 7 <120> TITLE OF INVENTION: RECOMBINANT FRAGMENTS OF THE HUMAN ACETYLCHOLINE RECEPTOR

AND THEIR USE

8 FOR TREATMENT OF MYASTHENIA GRAVIS
 10 <130> FILE REFERENCE: FUCHS=2A
 C/ 12 <140> CURRENT APPLICATION NUMBER: US/09/820,339
 C/ 12 <141> CURRENT FILING DATE: 1999-11-08
 12 <150> PRIOR APPLICATION NUMBER: 09/423,398
 13 <151> PRIOR FILING DATE: 1999-11-08
 15 <150> PRIOR APPLICATION NUMBER: PCT/IL98/00211
 16 <151> PRIOR FILING DATE: 1998-05-06
 18 <160> NUMBER OF SEQ ID NOS: 32
 20 <170> SOFTWARE: PatentIn version 3.0

22 <210> SEQ ID NO: 1

23 <211> LENGTH: 630

24 <212> TYPE: DNA

25 <213> ORGANISM: Homo sapiens

27 <400> SEQUENCE: 1

28 tccgaacatg agaccggctc ggtggcaaag ctattaaag actacagcag cgtggcg	60
30 ccagtggaaag accaccgcca ggtcgtggag gtcaccgtgg gcctgcagct gatacagctc	120
32 atcaatgtgg atgaagtaaa tcagatcgta acaaccaatg tgcgtctgaa acagaatgg	180
34 gtggattaca acctaataatg gaatccagat gactatggcg gtgtgaaaaa aattcacatt	240
36 ctttcagaaa agatctggcg cccagacctt gttctctata acgatgcaga tggtgacttt	300
38 gctattgtca agttcaccaa agtgctcctg cagtagactg gccacatcac gtggacacac	360
40 ccagccatct ttaaaagcta ctgtgagatc atcgtcaccc actttccctt tgatgaacag	420
42 aactgcagca tgaagctggg cacctggacc tacgacggct ctgtcgtggc catcaacccg	480
44 gaaagcggacc agccagacct gagcaacttc atggagagcg gggagtgggt gatcaaggag	540
46 tcccggggct ggaagcactc cgtagccat tcctgctgcc ccgacaccccc ctacctggac	600
48 atcacctacc acttcgtcat gcagcgcctg	630

51 <210> SEQ ID NO: 2

52 <211> LENGTH: 210

53 <212> TYPE: PRT

54 <213> ORGANISM: Homo sapiens

56 <400> SEQUENCE: 2

58 Ser Glu His Glu Thr Arg Leu Val Ala Lys Leu Phe Lys Asp Tyr Ser	
59 1 5 10 15	
61 Ser Val Val Arg Pro Val Glu Asp His Arg Gln Val Val Glu Val Thr	
62 20 25 30	
64 Ala Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp Glu Val Asn Gln	
65 35 40 45	
67 Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gln Trp Val Asp Tyr Asn	
68 50 55 60	
70 Leu Lys Trp Asn Pro Asp Asp Tyr Gly Gly Val Lys Lys Ile His Ile	
71 65 70 75 80	
73 Pro Ser Glu Lys Ile Trp Arg Pro Asp Leu Val Leu Tyr Asn Asn Ala	
74 85 90 95	

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/820,339

DATE: 07/27/2001

TIME: 14:22:07

Input Set : A:\ES.txt

Output Set: N:\CRF3\07272001\I820339.raw

76 Asp Gly Asp Phe Ala Ile Val Lys Phe Thr Lys Val Leu Leu Gln Tyr
 77 100 105 110
 79 Thr Gly His Ile Thr Trp Thr Pro Pro Ala Ile Phe Lys Ser Tyr Cys
 80 115 120 125
 82 Glu Ile Ile Val Thr His Phe Pro Phe Asp Glu Gln Asn Cys Ser Met
 83 130 135 140
 85 Lys Leu Gly Thr Trp Thr Tyr Asp Gly Ser Val Val Ala Ile Asn Pro
 86 145 150 155 160
 88 Glu Ser Asp Gln Pro Asp Leu Ser Asn Phe Met Glu Ser Gly Glu Trp
 89 165 170 175
 91 Val Ile Lys Glu Ser Arg Gly Trp Lys His Ser Val Thr Tyr Ser Cys
 92 180 185 190
 94 Cys Pro Asp Thr Pro Tyr Leu Asp Ile Thr Tyr His Phe Val Met Gln
 95 195 200 205
 97 Arg Leu
 98 210
 100 <210> SEQ ID NO: 3
 101 <211> LENGTH: 75
 102 <212> TYPE: DNA
 103 <213> ORGANISM: Homo sapiens
 105 <400> SEQUENCE: 3
 106 ggtgacatgg tagatctgcc acggccccagc tgcgtgactt tgggagttcc tttgtttct 60
 108 catctgcagg atgag 75
 111 <210> SEQ ID NO: 4
 112 <211> LENGTH: 25
 113 <212> TYPE: PRT
 114 <213> ORGANISM: Homo sapiens
 116 <400> SEQUENCE: 4
 118 Gly Asp Met Val Asp Leu Pro Arg Pro Ser Cys Val Thr Leu Gly Val
 119 1 5 10 15
 121 Pro Leu Phe Ser His Leu Gln Asp Glu
 122 20 25
 124 <210> SEQ ID NO: 5
 125 <211> LENGTH: 705
 126 <212> TYPE: DNA
 127 <213> ORGANISM: Homo sapiens
 129 <400> SEQUENCE: 5
 130 tcgcgaacatcg agaccgtct ggtggcaaag ctattaaag actacagcag cgtggcgg 60
 132 ccagtggaaag accaccgcca ggtcgtggag gtcaccgtgg gcctgcagct gatacagctc 120
 134 atcaatgtgg atgaagtaaa tcagatcgta acaaccaatg tgcgtctgaa acagggtgac 180
 136 atggtagatc tgccacgccc cagctgcgtg actttggag ttcccttgc ttctcatctg 240
 138 caggatgagc aatgggtgga ttacaaccta aaatggaatc cagatgacta tggcggtgtg 300
 140 aaaaaaaattc acattcccttc agaaaagatc tggcgcccag accttgttct ctataacgat 360
 142 gcagatggtg actttgttat tgtcaagtgc accaaagtgc tcctgcagta cactggccac 420
 144 atcacgtgga cacctccagc cattttaaa agctactgtg agatcatcgat caccacttt 480
 146 ccctttgatc aacagaactg cagcatgaag ctgggcacct ggacctacga cggctctgtc 540
 148 tgggccatca acccgaaag cgaccagcca gacctgagca acttcatgga gagcggggag 600
 150 tgggtgatca aggagtcccg gggctggaaag cactccgtga cctattctg ctgccccgac 660
 152 accccctacc tggacatcac ctaccacttc gtcatgcagc gcctg 705

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/820,339

DATE: 07/27/2001
TIME: 14:22:07

Input Set : A:\ES.txt
Output Set: N:\CRF3\07272001\I820339.raw

155 <210> SEQ ID NO: 6
 156 <211> LENGTH: 235
 157 <212> TYPE: PRT
 158 <213> ORGANISM: Homo sapiens
 160 <400> SEQUENCE: 6
 162 Ser Glu His Glu Thr Arg Leu Val Ala Lys Leu Phe Lys Asp Tyr Ser
 163 1 5 10 15
 165 Ser Val Val Arg Pro Val Glu Asp His Arg Gln Val Val Glu Val Thr
 166 20 25 30
 168 Ala Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp Glu Val Asn Gln
 169 35 40 45
 171 Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gly Asp Met Val Asp Leu
 172 50 55 60
 174 Pro Arg Pro Ser Cys Val Thr Leu Gly Val Pro Leu Phe Ser His Leu
 175 65 70 75 80
 177 Gln Asp Glu Gln Trp Val Asp Tyr Asn Leu Lys Trp Asn Pro Asp Asp
 178 85 90 95
 180 Tyr Gly Gly Val Lys Lys Ile His Ile Pro Ser Glu Lys Ile Trp Arg
 181 100 105 110
 183 Pro Asp Leu Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe Ala Ile Val
 184 115 120 125
 186 Lys Phe Thr Lys Val Leu Leu Gln Tyr Thr Gly His Ile Thr Trp Thr
 187 130 135 140
 189 Pro Pro Ala Ile Phe Lys Ser Tyr Cys Glu Ile Ile Val Thr His Phe
 190 145 150 155 160
 192 Pro Phe Asp Glu Gln Asn Cys Ser Met Lys Leu Gly Thr Trp Thr Tyr
 193 165 170 175
 195 Asp Gly Ser Val Val Ala Ile Asn Pro Glu Ser Asp Gln Pro Asp Leu
 196 180 185 190
 198 Ser Asn Phe Met Glu Ser Gly Glu Trp Val Ile Lys Glu Ser Arg Gly
 199 195 200 205
 201 Trp Lys His Ser Val Thr Tyr Ser Cys Cys Pro Asp Thr Pro Tyr Leu
 202 210 215 220
 204 Asp Ile Thr Tyr His Phe Val Met Gln Arg Leu
 205 225 230 235
 207 <210> SEQ ID NO: 7
 208 <211> LENGTH: 690
 209 <212> TYPE: DNA
 210 <213> ORGANISM: Homo sapiens
 212 <400> SEQUENCE: 7
 213 tccgaacatg agaccgtct ggtggcaaag ctattaaag actacagcag cgtggcg 60
 215 ccagtggaaag accaccgcca gtcgtggag gtcaccgtgg gcctgcagct gatacagctc 120
 217 atcaaatgtgg atgaagtaaa tcagatcgtg acaaccaatg tgctgtctgaa acagggtgac 180
 219 atggtagatc tgccacgccc cagctgcgtg actttggag ttccctttgtt ttctcatctg 240
 221 caggatgagc aatgggtgga ttacaaccta aaatggaatc cagatgacta tggcggtgtg 300
 223 aaaaaaattc acattcccttc agaaaagatc tggcgcccag accttgttct ctataacgt 360
 225 gcagatggtg actttgttat tgtcaagtgc accaaagtgc tcctgcagta cactggccac 420
 227 atcacgtgga cacctccagc catctttaaa agctactgtg agatcatcgt caccacttt 480
 229 ccctttgatg aacagaactg cagcatgaag ctggcacct ggacctacga cggtctgtc 540

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/820,339

DATE: 07/27/2001
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Input Set : A:\ES.txt
Output Set: N:\CRF3\07272001\I820339.raw

231 gtggccatca acccgaaag cgaccagcca gacctgagca acttcatgga gagccccggag 600
 233 tgggtgatca aggagtcccg gggctgaaag cactccgtga cctattcctg ctgccccgac 660
 235 acccccctacc tggacatcac ctaccacttc 690
 238 <210> SEQ ID NO: 8
 239 <211> LENGTH: 230
 240 <212> TYPE: PRT
 241 <213> ORGANISM: Homo sapiens
 243 <400> SEQUENCE: 8
 245 Ser Glu His Glu Thr Arg Leu Val Ala Lys Leu Phe Lys Asp Tyr Ser
 246 1 5 10 15
 248 Ser Val Val Arg Pro Val Glu Asp His Arg Gln Val Val Glu Val Thr
 249 20 25 30
 251 Ala Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp Glu Val Asn Gln
 252 35 40 45
 254 Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gly Asp Met Val Asp Leu
 255 50 55 60
 257 Pro Arg Pro Ser Cys Val Thr Leu Gly Val Pro Leu Phe Ser His Leu
 258 65 70 75 80
 260 Gln Asp Glu Gln Trp Val Asp Tyr Asn Leu Lys Trp Asn Pro Asp Asp
 261 85 90 95
 263 Tyr Gly Gly Val Lys Lys Ile His Ile Pro Ser Glu Lys Ile Trp Arg
 264 100 105 110
 266 Pro Asp Leu Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe Ala Ile Val
 267 115 120 125
 269 Lys Phe Thr Lys Val Leu Leu Gln Tyr Thr Gly His Ile Thr Trp Thr
 270 130 135 140
 272 Pro Pro Ala Ile Phe Lys Ser Tyr Cys Glu Ile Ile Val Thr His Phe
 273 145 150 155 160
 275 Pro Phe Asp Glu Gln Asn Cys Ser Met Lys Leu Gly Thr Trp Thr Tyr
 276 165 170 175
 278 Asp Gly Ser Val Val Ala Ile Asn Pro Glu Ser Asp Gln Pro Asp Leu
 279 180 185 190
 281 Ser Asn Phe Met Glu Ser Gly Glu Trp Val Ile Lys Glu Ser Arg Gly
 282 195 200 205
 284 Trp Lys His Ser Val Thr Tyr Ser Cys Cys Pro Asp Thr Pro Tyr Leu
 285 210 215 220
 287 Asp Ile Thr Tyr His Phe
 288 225 230
 290 <210> SEQ ID NO: 9
 291 <211> LENGTH: 20
 292 <212> TYPE: DNA
 C--> 293 <213> ORGANISM: Artificial synthetic
 W--> 295 <220> FEATURE:
 W--> 295 <223> OTHER INFORMATION: *synthetic* goes on <223> line.
 295 <400> SEQUENCE: 9
 296 ccggatccga acatgagacc
 299 <210> SEQ ID NO: 10
 300 <211> LENGTH: 23
 301 <212> TYPE: DNA

(global error)

invalid - see item 10 on Error Summary Sheet

Synthetic goes on <223> line.

=====

20

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/820,339

DATE: 07/27/2001
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Input Set : A:\ES.txt
Output Set: N:\CRF3\07272001\I820339.raw

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C--> 302 <213> ORGANISM: Artificial synthetic
W--> 304 <220> FEATURE:
W--> 304 <223> OTHER INFORMATION:
 304 <400> SEQUENCE: 10
 305 cgaattcca ggcgctgcat gac
 308 <210> SEQ ID NO: 11
 309 <211> LENGTH: 26
 310 <212> TYPE: DNA
C--> 311 <213> ORGANISM: Artificial synthetic
W--> 313 <220> FEATURE:
W--> 313 <223> OTHER INFORMATION:
 313 <400> SEQUENCE: 11
 314 cgaattctg gaggtgtcca cgtgat
 317 <210> SEQ ID NO: 12
 318 <211> LENGTH: 23
 319 <212> TYPE: DNA
C--> 320 <213> ORGANISM: Artificial synthetic
W--> 322 <220> FEATURE:
W--> 322 <223> OTHER INFORMATION:
 322 <400> SEQUENCE: 12
 323 ccggatccgc catcttaaa agc
 326 <210> SEQ ID NO: 13
 327 <211> LENGTH: 25
 328 <212> TYPE: DNA
C--> 329 <213> ORGANISM: Artificial synthetic
W--> 331 <220> FEATURE:
W--> 331 <223> OTHER INFORMATION:
 331 <400> SEQUENCE: 13
 332 ggccatgggc tccgaacatg agacc
 335 <210> SEQ ID NO: 14
 336 <211> LENGTH: 29
 337 <212> TYPE: DNA
C--> 338 <213> ORGANISM: Artificial synthetic
W--> 340 <220> FEATURE:
W--> 340 <223> OTHER INFORMATION:
 340 <400> SEQUENCE: 14
 341 ccggatcctc aaaagtgrta ggtgatrtc
 344 <210> SEQ ID NO: 15
 345 <211> LENGTH: 24
 346 <212> TYPE: DNA
C--> 347 <213> ORGANISM: Artificial synthetic
W--> 349 <220> FEATURE:
W--> 349 <223> OTHER INFORMATION:
 349 <400> SEQUENCE: 15
 350 cgctatgggg ctgcttgtt acag
 353 <210> SEQ ID NO: 16
 354 <211> LENGTH: 24
 355 <212> TYPE: DNA
C--> 356 <213> ORGANISM: Artificial synthetic

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FYI →

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/820,339

DATE: 07/27/2001
TIME: 14:22:08

Input Set : A:\ES.txt
Output Set: N:\CRF3\07272001\I820339.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:293 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:295 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:295 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:302 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:304 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:304 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:311 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:313 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:313 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:320 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:322 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:322 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:329 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:331 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:331 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:338 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:340 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:340 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:347 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:349 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:349 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:356 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:358 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:358 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:365 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:367 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:367 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:374 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:376 M:258 W: Mandatory Feature missing, <220> FEATURE:
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L:385 M:258 W: Mandatory Feature missing, <220> FEATURE:
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L:392 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:394 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:394 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:401 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:403 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:403 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:410 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:412 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:412 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:419 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:421 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:421 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:428 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/820,339

DATE: 07/27/2001

TIME: 14:22:08

Input Set : A:\ES.txt

Output Set: N:\CRF3\07272001\I820339.raw

L:430 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:430 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:437 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:439 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:439 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:446 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:448 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:448 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:455 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:457 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:457 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:464 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:466 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:466 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:473 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:475 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:475 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:482 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:484 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:484 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:491 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
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